

#4

TOREKE

PCT09

RAW SEQUENCE LISTING

DATE: 09/13/2001

PATENT APPLICATION: US/09/914,152

TIME: 17:18:01

Input Set : A:\2139.25 Sequence.txt

Output Set: N:\CRF3\09132001\I914152.raw

3 <110> APPLICANT: Hisashi NARIMATSU et al.:
 5 <120> TITLE OF INVENTION: NOVEL POLYPEPTIDES
 7 <130> FILE REFERENCE: 11192US1
 9 <140> CURRENT APPLICATION NUMBER: US/09/914,152
 10 <141> CURRENT FILING DATE: 2001-08-24
 12 <150> PRIOR APPLICATION NUMBER: JP 99/47571
 13 <151> PRIOR FILING DATE: 2000-02-25
 15 <160> NUMBER OF SEQ ID NOS: 25
 17 <170> SOFTWARE: PatentIn Ver. 2.0
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 310
 21 <212> TYPE: PRT
 22 <213> ORGANISM: Homo sapiens
 24 <400> SEQUENCE: 1

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31	Glu	Gln	Ser	Phe	Val	Tyr	Lys	Lys	Asp	Gly	Asn	Phe	Leu	Lys	Leu	Pro
32			35				40				45					
34	Asp	Thr	Asp	Cys	Arg	Gln	Thr	Pro	Pro	Phe	Leu	Val	Leu	Leu	Val	Thr
35	50				55			60								
37	Ser	Ser	His	Lys	Gln	Leu	Ala	Glu	Arg	Met	Ala	Ile	Arg	Gln	Thr	Trp
38	65			70			75					80				
40	Gly	Lys	Glu	Arg	Met	Val	Lys	Gly	Lys	Gln	Leu	Lys	Thr	Phe	Phe	Leu
41				85			90				95					
43	Leu	Gly	Thr	Thr	Ser	Ser	Ala	Ala	Glu	Thr	Lys	Glu	Val	Asp	Gln	Glu
44			100				105				110					
46	Ser	Gln	Arg	His	Gly	Asp	Ile	Ile	Gln	Lys	Asp	Phe	Leu	Asp	Val	Tyr
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49	Tyr	Asn	Leu	Thr	Leu	Lys	Thr	Met	Met	Gly	Ile	Glu	Trp	Val	His	Arg
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52	Phe	Cys	Pro	Gln	Ala	Ala	Phe	Val	Met	Lys	Thr	Asp	Ser	Asp	Met	Phe
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56			165				170				175					
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59		180				185			190							
61	Gln	Pro	Phe	Ser	Lys	Trp	Phe	Val	Ser	Lys	Ser	Glu	Tyr	Pro	Trp	Asp
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64	Arg	Tyr	Pro	Pro	Phe	Cys	Ser	Gly	Thr	Gly	Tyr	Val	Phe	Ser	Gly	Asp
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ENTERED

p.5

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106  tggagcattc tacactgaca gttctttgag acaatttcc tcttggcatt tacactgtgg 360
108  ctttagcttt caaaccagag gttcctotta ccagcaaaa a atg gct ttc ccg aag 416
109                                     Met Ala Phe Pro Lys
110                                     1 5
112  atg aga ttg atg tat att tgc ctt ctg gtt ctg ggg gct ctt tgt ttg 464
113  Met Arg Leu Met Tyr Ile Cys Leu Leu Val Leu Gly Ala Leu Cys Leu
114          10          15          20
116  tat ttt agc atg tac agt cta aat cct ttc aaa gaa cag tcc ttt gtt 512
117  Tyr Phe Ser Met Tyr Ser Leu Asn Pro Phe Lys Glu Gln Ser Phe Val
118          25          30          35
120  tac aag aaa gac ggg aac ttc ctt aag ctg cca gat aca gac tgc agg 560
121  Tyr Lys Lys Asp Gly Asn Phe Leu Lys Leu Pro Asp Thr Asp Cys Arg
122          40          45          50
124  cag aca cct ccc ttc ctg gtc ctg ctg gtt acc tca tcc cac aaa cag 608
125  Gln Thr Pro Pro Phe Leu Val Leu Leu Val Thr Ser Ser His Lys Gln
126          55          60          65
128  ttg gct gag cgc atg gcc atc cgg cag acg tgg ggg aaa gag agg atg 656
129  Leu Ala Glu Arg Met Ala Ile Arg Gln Thr Trp Gly Lys Glu Arg Met
130          70          75          80          85
132  gtg aag gga aag cag ctg aag aca ttc ttc ctg ctg ggg acc acc agc 704
133  Val Lys Gly Lys Gln Leu Lys Thr Phe Phe Leu Leu Gly Thr Thr Ser
134          90          95          100
136  agt gca gcg gaa acg aaa gag gtg gac cag gag agc cag cga cac ggg 752
137  Ser Ala Ala Glu Thr Lys Glu Val Asp Gln Glu Ser Gln Arg His Gly
138          105          110          115
140  gac att atc cag aag gat ttc cta gac gtc tat tac aat ctg acc ctg 800
141  Asp Ile Ile Gln Lys Asp Phe Leu Asp Val Tyr Tyr Asn Leu Thr Leu
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144  aag acc atg atg ggc ata gaa tgg gtc cat cgc ttt tgt cct cag gcg 848

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149  Ala Phe Val Met Lys Thr Asp Ser Asp Met Phe Ile Asn Val Asp Tyr
150  150                      155                      160                      165
152  ctg act gaa ctg ctt ctg aag aaa aac aga aca acc agg ttt ttc act 944
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154      170                      175                      180
156  ggc ttc ttg aaa ctc aat gag ttt ccc atc agg cag cca ttc agc aag 992
157  Gly Phe Leu Lys Leu Asn Glu Phe Pro Ile Arg Gln Pro Phe Ser Lys
158      185                      190                      195
160  tgg ttt gtc agt aaa tct gaa tat ccg tgg gac agg tac cca cca ttc 1040
161  Trp Phe Val Ser Lys Ser Glu Tyr Pro Trp Asp Arg Tyr Pro Pro Phe
162      200                      205                      210
164  tgc tcc ggc acc ggc tac gtg ttt tct ggc gac gtg gcg agt cag gtg 1088
165  Cys Ser Gly Thr Gly Tyr Val Phe Ser Gly Asp Val Ala Ser Gln Val
166      215                      220                      225
168  tac aat gtc tcc aag agc gtc cca tac att aaa ctg gaa gac gtg ttt 1136
169  Tyr Asn Val Ser Lys Ser Val Pro Tyr Ile Lys Leu Glu Asp Val Phe
170      230                      235                      240                      245
172  gtg ggg ctc tgc ctc gaa agg ctg aac atc aga ttg gag gag ctc cac 1184
173  Val Gly Leu Cys Leu Glu Arg Leu Asn Ile Arg Leu Glu Glu Leu His
174      250                      255                      260
176  tcc cag ccg acc ttt ttt cca ggg ggc tta cgc ttc tcc gta tgc ctc 1232
177  Ser Gln Pro Thr Phe Phe Pro Gly Gly Leu Arg Phe Ser Val Cys Leu
178      265                      270                      275
180  ttc agg agg atc gtg gcc tgc cac ttc atc aag cct cgg act ctc ttg 1280
181  Phe Arg Arg Ile Val Ala Cys His Phe Ile Lys Pro Arg Thr Leu Leu
182      280                      285                      290
184  gac tac tgg cag gct cta gag aat tcc cgg ggg gaa gat tgt ccg cct 1328
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188  gtc tgaggggagc ccagaggcac atccggacaa gtttcagata acccgtgggg 1381
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190  310
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234 ttaatttttt actttaccag actttacttt gtactcagag aagaggcctc acatggctgt 2701
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Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

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L:9 M:270 C: Current Application Number differs, Replaced Application Number

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:795 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16

L:822 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17

L:844 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18

L:876 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19